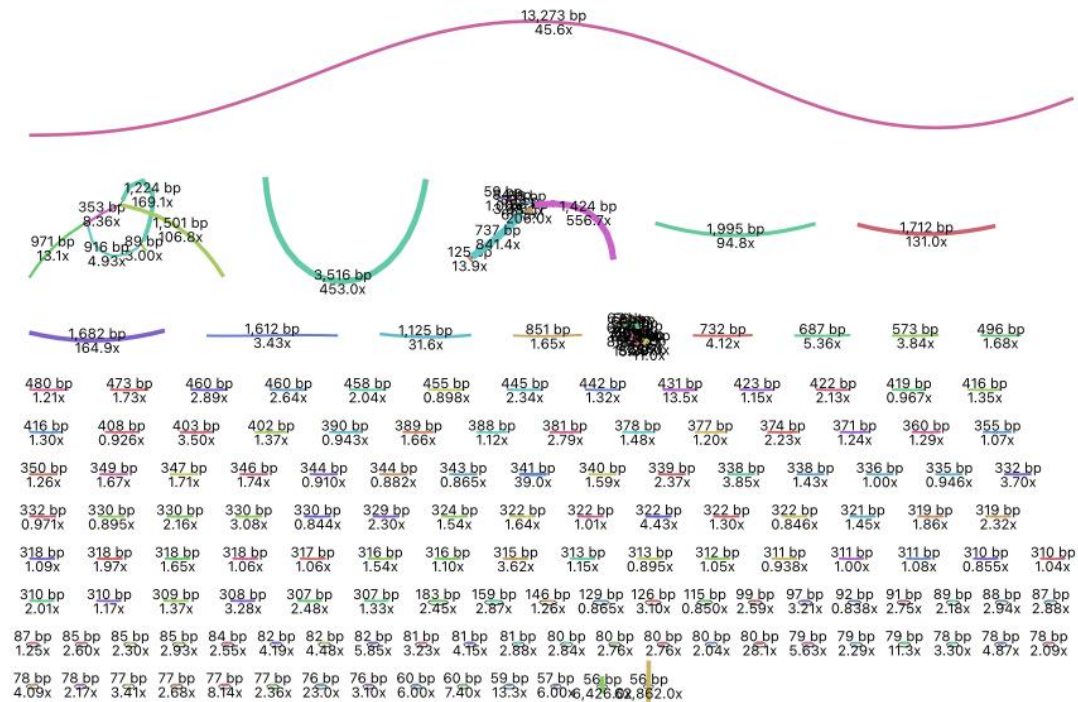




Supplementary figure S1: De novo assembly graph showing recovery of the hMPV genome. The assembly graph was generated from SPAdes and visualized using Bandage. Nodes represent assembled contigs, with lengths and average sequencing depth indicated. A single dominant contig of 13,273 bp of the near-complete hMPV genome is seen at ~ 45.6× coverage, with no evident branching, indicating a well-supported unambiguous assembly. Numerous shorter, low-coverage contigs represent other sequences of the metagenome.